

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

These amendments introduce no new matter and support for the amendment is replete throughout the specification and claims as originally filed. These amendments are made without prejudice and are not to be construed as abandonment of the previously claimed subject matter, or agreement with any objection or rejection of record.

Listing of Claims:

Claims 1 to 30 (Cancelled).

31. (Currently amended) A composition comprising a protein, wherein the protein comprises two or more different redox active amino acids selected from the group consisting of: a 3,4-dihydroxy-L-phenylalanine (DHP), a 3,4,5-trihydroxy-L-phenylalanine, a 3-nitro-tyrosine, a 4-nitro-phenylalanine, and a 3-thiol-tyrosine;

~~the composition further comprising:~~

- ~~i) at least one orthogonal tRNA (O-tRNA), wherein the O-tRNA comprises or is encoded by a polynucleotide sequence as set forth in SEQ ID NO: 2;~~
- ~~ii) at least one orthogonal aminoacyl-tRNA-synthetase (O-RS) comprising or derived from an RS selected from the group consisting of: an *Archaeoglobus fulgidus* synthetase, a *Methanosarcina mazei* synthetase, a *Methanobacterium thermoautotrophicum* synthetase, and a *Pyrococcus horikoshii* synthetase, wherein the O-RS preferentially aminoacylates the O-tRNA with one of the redox active amino acids; and~~
- ~~iii) a nucleic acid that encodes the protein, wherein the nucleic acid comprises at least two selector codons that are recognized by the O-tRNA.~~

32. (Cancelled)

33. (Cancelled)

34. **(Original)** The composition of claim 31, wherein the composition comprises a pharmaceutically acceptable carrier.

35. **(Previously presented)** The composition of claim 31, wherein the protein further comprises at least one unnatural amino acid that is not a 3,4-dihydroxy-L-phenylalanine (DHP), a 3,4,5-trihydroxy-L-phenylalanine, a 3-nitro-tyrosine, a 4-nitro-phenylalanine, or a 3-thiol-tyrosine.

36. **(Cancelled)**

37. **(Cancelled)**

38. **(Cancelled)**

39. **(Previously presented)** The composition of claim 31, wherein the protein comprises a myoglobin polypeptide or a portion thereof.

40. **(Cancelled)**

41. **(Previously presented)** The composition of claim 31, wherein the protein is capable of undergoing oxidation.

42. **(Previously presented)** The composition of claim 31, wherein the protein is capable of undergoing (i) oxidation or (ii) a shift in reductive peak potential as measured by voltammetric response in comparison to a corresponding protein that lacks said at least two redox active amino acids, and wherein said oxidation or shift in reductive peak potential require said at least two redox active amino acids.

43. **(Previously presented)** The composition of claim 31, wherein at least one of said two or more redox active amino acids is 3,4-dihydroxy-L-phenylalanine (DHP).

44. **(Previously presented)** The composition of claim 31, wherein the redox active amino acid is a redox catalyst.

45. **(Cancelled).**

46. **(Previously presented)** The composition of claim 31, further comprising an O-RS comprising an amino acid sequence comprising SEQ ID NO.: 1.

47. **(Currently amended)** A composition comprising:

a protein, wherein the protein comprises at least one ~~two or more~~ redox active amino acid selected from the group consisting of: a 3,4-dihydroxy-L-phenylalanine (DHP), a 3,4,5-trihydroxy-L-phenylalanine, a 3-nitro-tyrosine, a 4-nitro-phenylalanine, and a 3-thiol-tyrosine,

an O-tRNA,

an aminoacyl-tRNA synthetase comprising an amino acid sequence at least 90% identical to SEQ ID NO: 1 that preferentially aminoacylates the O-tRNA with a redox active amino acid selected from the group,

and a nucleic acid encoding a polypeptide of interest, said nucleic acid comprising at least two selector codons that are recognized by the O-tRNA.

48. (New) The composition of claim **47**, wherein the synthetase further comprises: a Leu amino acid in a position of the O-RS corresponding to Tyr32 of SEQ ID NO: 4, a Ser amino acid residue in a position of the O-RS corresponding to Ala67 of SEQ ID NO: 4, an Asn amino acid residue in a position of the O-RS corresponding to His70 of SEQ ID NO: 4 or a Gln residue in a position of the O-RS corresponding to Ala167 of SEQ ID NO: 4, and SEQ ID NO: 4 is the wild type sequence.

49. (New) The composition of claim **47**, wherein the synthetase further comprises: a Leu amino acid in a position of the O-RS corresponding to Tyr32 of SEQ ID NO: 4, a Ser amino acid residue in a position of the O-RS corresponding to Ala67 of SEQ ID NO: 4, an Asn amino acid residue in a position of the O-RS corresponding to His70 of SEQ ID NO: 4, and a Gln residue in a position of the O-RS corresponding to Ala167 of SEQ ID NO: 4, and SEQ ID NO: 4 is the wild type sequence.

50. (New) The composition of claim **47**, wherein the redox amino acid is a meta-substituted amino acid selected from the group consisting of: 3,4-dihydroxy-L-phenylalanine (DHP), 3,4,5-trihydroxy-L-phenylalanine and 4-nitro-phenylalanine.

51. (New) The composition of claim **50**, wherein the synthetase further comprises: a Leu amino acid in a position of the O-RS corresponding to Tyr32 of SEQ ID NO: 4, a Ser amino acid residue in a position of the O-RS corresponding to Ala67 of SEQ ID NO: 4, an Asn amino acid residue in a position of the O-RS corresponding to His70 of SEQ

ID NO: 4 or a Gln residue in a position of the O-RS corresponding to Ala167 of SEQ ID NO: 4, and SEQ ID NO: 4 is the wild type sequence.

52. (New) The composition of claim **47**, wherein the redox amino acid is a para-substituted amino acid selected from the group consisting of 3,4-dihydroxy-L-phenylalanine (DHP), 3,4,5-trihydroxy-L-phenylalanine, 3-nitro-tyrosine, and 3-thiol-tyrosine.

53. (New) The composition of claim **52**, wherein the synthetase further comprises: a Leu amino acid in a position of the O-RS corresponding to Tyr32 of SEQ ID NO: 4.

54. (New) The composition of claim **47**, wherein the protein comprises two or more of the redox active amino acids.

55. (New) The composition of claim **47**, wherein the synthetase comprises an amino acid sequence at least 95% identical to SEQ ID NO: 1.

56. (New) The composition of claim **31** further comprising:
at least one orthogonal tRNA (O-tRNA), wherein the O-tRNA comprises or is encoded by a polynucleotide sequence as set forth in SEQ ID NO: 2, or a conservative variant thereof.

57. (New) The composition of claim **31** further comprising:
at least one orthogonal aminoacyl-tRNA synthetase (O-RS) comprising a synthetase selected from the group consisting of: an *Archaeoglobus fulgidus* synthetase, a *Methanosarcina mazei* synthetase, a *Methanobacterium thermoautotrophicum* synthetase, and a *Pyrococcus horikoshii* synthetase, wherein the O-RS preferentially aminoacylates an O-tRNA with one of the redox active amino acids

58. (New) The composition of claim **31** further comprising:
a nucleic acid that encodes the protein, wherein the nucleic acid comprises at least two selector codons that are recognized by an O-tRNA.